

	Type	L #	Hits	Search Text
1	BRS	L1	3	"5849882"
2	BRS	L2	7989	(bioactive) [AB]
3	BRS	L3	1440	(bioactive and peptides) [AB]
4	BRS	L4	91	(bioactive and peptides and fragment) [AB]
5	BRS	L5	417	(bioactive near5 peptides) [AB]
6	BRS	L6	319	(bioactive near2 peptides) [AB]
7	BRS	L7	15	((bioactive near2 peptides) and hydrolysis) [AB]

Database :        Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1523	97.3	300	1	US-08-469-665-2	Sequence 2, Appli	
2	1523	97.3	300	2	US-09-038-596-2	Sequence 2, Appli	
3	1523	97.3	300	5	PCT-US95-00421-2	Sequence 2, Appli	
4	707	45.1	376	3	US-09-091-725-15	Sequence 15, Appl	
5	583	37.2	335	2	US-08-761-344-2	Sequence 2, Appli	
6	238.5	15.2	341	4	US-09-252-991A-21448	Sequence 21448, A	
7	229.5	14.7	340	4	US-09-543-681A-5778	Sequence 5778, Ap	
8	225.5	14.4	162	4	US-09-248-796A-17986	Sequence 17986, A	
9	213.5	13.6	165	4	US-09-248-796A-17985	Sequence 17985, A	
10	207	13.2	330	1	US-08-410-167A-4	Sequence 4, Appli	
11	207	13.2	330	2	US-08-898-560-1	Sequence 1, Appli	
12	206	13.2	330	3	US-09-101-126-1	Sequence 1, Appli	
13	197.5	12.6	342	4	US-09-489-039A-13653	Sequence 13653, A	
14	197	12.6	353	4	US-09-328-352-4226	Sequence 4226, Ap	

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			Query				
No.	Score	Match	Length	DB	ID	Description	
1	1566	100.0	300	15	US-10-041-018-46	Sequence 46, Appl	
2	1550	99.0	304	9	US-09-925-302-614	Sequence 614, App	
3	1550	99.0	304	10	US-09-925-302-614	Sequence 614, App	
4	928	59.3	338	15	US-10-041-018-24	Sequence 24, Appl	
5	928	59.3	338	15	US-10-041-018-77	Sequence 77, Appl	
6	862.5	55.1	335	15	US-10-041-018-23	Sequence 23, Appl	
7	862.5	55.1	335	15	US-10-041-018-76	Sequence 76, Appl	
8	806.5	51.5	303	15	US-10-041-018-34	Sequence 34, Appl	
9	797.5	50.9	428	15	US-10-369-493-4221	Sequence 4221, Ap	
10	792	50.6	348	15	US-10-369-493-12405	Sequence 12405, A	
11	725	46.3	452	15	US-10-369-493-12982	Sequence 12982, A	
12	707	45.1	376	15	US-10-001-192A-15	Sequence 15, Appl	
13	613.5	39.2	319	15	US-10-369-493-12991	Sequence 12991, A	

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length	Length			
1	1566	100.0	300	1	GGPP_HUMAN	Q95749	h geranylge
2	1558	99.5	300	2	Q6NW19	Q6nw19	homo sapien
3	1516	96.8	294	1	GGPP_BOVIN	P56966	b geranylge
4	1490	95.1	300	2	Q6F596	Q6f596	rattus norv
5	1476	94.3	300	1	GGPP_MOUSE	Q9wtn0	m geranylge
6	1322	84.4	327	2	Q7ZTY0	Q7zty0	brachydanio
7	1163	74.3	236	2	Q9CZZ6	Q9czz6	mus musculu
8	928	59.3	338	2	O61539	O61539	drosophila
9	928	59.3	338	2	Q9VS54	Q9vs54	drosophila
10	888	56.7	357	2	Q7QI19	Q7qii9	anopheles g
11	862.5	55.1	335	2	O61538	O61538	drosophila
12	819	52.3	335	2	Q86F69	Q86f69	schistosoma
13	806.5	51.5	303	2	Q9P885	Q9p885	mucor circi
14	802	51.2	340	2	Q672V6	Q672v6	aspergillus
15	797.5	50.9	428	1	GGPP_NEUCR	P24322	n geranylge
16	794.5	50.7	396	2	Q874I1	Q874i1	emericella
17	794	50.7	375	2	Q9C452	Q9c452	penicillium

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	1566	100.0	300	3	AAV68909		Aay68909 A geranyl	
2	1566	100.0	300	8	ADJ10383		Adj10383 Human ger	
3	1566	100.0	300	8	ADM98626		Adm98626 Geranylge	
4	1550	99.0	304	3	AAB58276		Aab58276 Lung canc	
5	1523	97.3	300	2	AAW59753		Aaw59753 Human ger	
6	1523	97.3	300	2	AAV27005		Aay27005 Human ger	
7	1519	97.0	300	2	AAR97565		Aar97565 Human ger	
8	1244.5	79.5	320	4	AAU30743		Aau30743 Novel hum	
9	928	59.3	338	4	ABB60947		Abb60947 Drosophil	
10	928	59.3	338	8	ADM98657		Adm98657 Geranylge	
11	928	59.3	338	8	ADM98604		Adm98604 Geranylge	
12	862.5	55.1	335	8	ADM98656		Adm98656 Geranylge	
13	862.5	55.1	335	8	ADM98603		Adm98603 Geranylge	